**AMENDMENTS TO THE CLAIMS:**

This listing of claims will replace all prior versions and listings of claims in the application:

**LISTING OF CLAIMS:**

Amendments shown by strikethrough (for deleted matter) or underlining (for added matter).

1. (currently amended) A m~~M~~ethod for determining the presence of genetic element ~~such as nucleotide repeat or a marker for microbial typing~~ in a nucleic acid sample, which method comprises the steps of:

a) providing the ~~a~~ nucleic acid sample comprising the ~~a~~ genetic element(s);

b) providing an oligonucleotide that is completely or partially complementary to a region comprising the genetic element of said nucleic acid sample;

c) annealing said oligonucleotide to said nucleic acid sample;

d) ligating at least two of said oligonucleotides annealed to said nucleic acid sample to each other using a ligase enzyme; and

e) detecting pyrophosphate ~~a ligation by product~~ to determine whether a ligation reaction has occurred, as a measure of the presence of the genetic element,

wherein steps a)-e) are performed simultaneously or subsequently or in any combination of subsequent steps.

2. (currently amended) A m~~M~~ethod for analysing the number of nucleotide repeats in a nucleic acid sample, which method comprises the steps of:

a) providing the ~~a~~ nucleic acid sample potentially comprising a nucleotide repeat;

b) providing an oligonucleotide complementary to said nucleotide repeat;

c) annealing said oligonucleotide to said nucleic acid sample;

d) ligating at least two of said oligonucleotides annealed to said nucleic acid sample to each other using a ligase enzyme; and

e) detecting pyrophosphate ~~a ligation by product~~ to determine whether a ligation reaction has occured,

wherein steps a)-e) are performed simultaneously or subsequently or in any combination of subsequent steps.

3. (currently amended) A m~~M~~ethod for analysing the number of nucleotide repeats in a nucleic acid sample, which method comprises the steps of:

a) providing the ~~a~~ nucleic acid sample potentially comprising a nucleotide repeat;

b) providing an oligonucleotide complementary to said nucleotide repeat;

c) annealing said oligonucleotide to said nucleic acid sample;

d) ligating at least two of said oligonucleotides annealed to said nucleic acid sample to each other using a ligase enzyme;

e) converting pyrophosphate ~~a ligation by product~~ into ATP; and

f) detecting said ATP to determine whether a ligation reaction has occured,

wherein steps a)-f) are performed simultaneously or subsequently or in any combination of subsequent steps.

4. (currently amended) A m~~M~~ethod for analysing the number of nucleotide repeats in a nucleic acid sample, which method comprises the steps of:

a) providing the ~~a~~ nucleic acid sample potentially comprising a nucleotide repeat;

b) providing an oligonucleotide complementary to said nucleotide repeat;

c) annealing said oligonucleotide to said nucleic acid sample;

d) ligating at least two of said oligonucleotides annealed to said nucleic acid sample to each other using a ligase enzyme;

e) converting pyrophosphate ~~a ligation by product~~ into ATP; and

f) detecting said ATP by a luciferase-based assay as a measure of whether a ligation reaction has occured,

wherein steps a)-f) are performed simultaneously or subsequently or in any combination of subsequent steps.

5. (currently amended) A m~~M~~ethod for microbial typing of a nucleic acid sample, which method comprises the steps of:

a) providing the ~~a~~ nucleic acid sample comprising at least one marker for microbial typing;

b) providing an oligonucleotide that is completely or partially complementary to a region comprising a marker for microbial typing of said nucleic acid sample;

c) annealing said oligonucleotide(s) to said nucleic acid sample;

d) ligating at least two of said oligonucleotides annealed to said nucleic acid sample to each other using a ligase enzyme; and

e) detecting pyrophosphate ~~a ligation by product~~ to determine whether a ligation reaction has occurred;

f) comparing the ligation pattern of the sample with a reference pattern, in order to determine the microbial type,

wherein steps a)-e) are performed simultaneously or subsequently or in any combination of subsequent steps.

6. (currently amended) The m~~M~~ethod according to any one of claims 1-5 wherein one of the oligonucleotides in step b) is adapted to anneal immediately outside the repeated sequence.

7. (cancelled)

8. (currently amended) The m~~M~~ethod according to any one of claims 1-7 wherein step d) is performed employing a $NAD^+$-dependent DNA-ligase.

9. (currently amended) The m~~M~~ethod according to any one of claims 1-8 wherein step e) is performed employing a pyruvate phosphate dikinase.

10. (currently amended) The m~~M~~ethod according to any one of claims 1-6, wherein step d) is performed employing an ATP-dependent ligase, and apyrase is added to the ligation mixture of step d) before, during or after ligation in order to reduce excess amounts of DNA ligase substrate.

11. (currently amended) The m~~M~~ethod according to claim 10, wherein the ATP dependent ligase is T4 DNA ligase.

12. (currently amended) The m~~M~~ethod according to claim 10 or 11, wherein dATP is used as a substrate for the ATP dependent ligase in step d).

13. (cancelled)

14. (currently amended) The m~~M~~ethod according to any one of claims 1-6 or 10-13, wherein step e) is performed employing a ATP-sulfurylase.

15. (currently amended) The m~~M~~ethod according to any one of claims 1-14, wherein the oligonucleotide employed is a mono-, di- or multimer of the repeat in itself.

16. (currently amended) The m~~M~~ethod according to any one of claims 1-14, wherein the oligonucleotides are complementary to, but that are out of phase with, said nucleotide repeat.

17. (currently amended) The m~~M~~ethod according to claim 16, further comprising a step wherein unannealed oligonucleotides are removed after the detection by using an exonuclease.

18. (currently amended) The m~~M~~ethod according to claim 16, further comprising a step wherein unannealed oligonucleotides are inactivated after the detection by using a phosphatase.

19. (currently amended) The m~~M~~ethod according to any one of claims 1-18, wherein the nucleic acid sample is immobilised on a support.

20. (currently amended) The m~~M~~ethod according to claim 19, further comprising a step wherein unannealed oligonucleotides are removed after the detection by washing.

21. (currently amended) The m~~M~~ethod according to any one of claims 1-20, preceeded by a step wherein the nucleic acid sample is amplified.

22. (currently amended) The m~~M~~ethod according to any one of claims 1-21, wherein the luciferase-based assay is a luminometric assay.

23. (currently amended) The m~~M~~ethod according to any one of claims 1-22, wherein the light that is produced in the luciferase reaction is enzymatically turned off after an initial level of produced light has been reached.

24. (currently amended) The m~~M~~ethod according to claim 23, wherein light production is turned off by the addition of apyrase.

25. (currently amended) The m~~M~~ethod according to any one of claims 1-24 where oligonucleotides complementary to a region outside that to be analyzed are used to generate a signal by ligation or primer extension that can be used to normalize the signal obtained from the region to be analyzed.

26-34. (cancelled)